REMARKS UNDER 37 CFR § 1.111

Formal Matters

Claims 1-11, 22, 27-28, 31-37, 41-44 and 47-49 are pending after entry of the amendments set forth herein.

Claim 46 has been canceled without prejudice.

Claims 1-11, 22, 27-28, 31-37, 41-44 and 46-49 were examined. Claims 1-11, 22, 27-28, 31-37, 41-44 and 46-49 were rejected.

Applicant respectfully requests reconsideration of the application in view of the amendments and remarks made herein.

No new matter has been added.

The Office Action

Claim Objection

Claim 46 was provisionally objected to as being a substantial duplicate of claim 42. In response thereto, Applicant has canceled claim 46 above, without prejudice. Accordingly, the Examiner is respectfully requested to reconsider and withdraw this provisional ground of objection as being no longer appropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Zhou et al. in view of Markowitz et al. and Cracauer et al.)

Claims 1-11, 22, 27-28, 31-37, 41-44 and 46-49 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Zhou et al., USPAP 2003/0120432 A1 in view of Markowitz et al., USPAP 2003/0100999 and Cracauer et al., USPAP 2007/0178474.

The Examiner asserted: "Zhou et al. describe the genomic portal system receives user-selected identifiers including sequence information, the system verifies probes corresponding to identifiers and generates a custom probe array design (paragraphs 0006 and 0008) and constructing and arranging

arrays to detect and/or measure any one gene expression (paragraph 0007) which represent providing parameters to the vendor who curates the sequence and selects the probes specific for the curated sequence as mention in paragraph 0005...". Applicant respectfully traverses. It is respectfully submitted that paragraph [0005] discloses nothing about curating, as it is only a summarization of uses of web portal processes where, in some implementations, the user selects probe-set identifiers.

The Examiner further asserted that Zhou et al. describe further generation including modifying or rejecting one or more user-selected probe array format factors including user-selected probe set identifiers and displaying this information to the user (paragraph 0010), which the Examiner interpreted to represent the vendor selecting at least one probe specific for the curated gene sequence. Applicant respectfully traverses. It is respectfully submitted that Zhou et al. does not teach or suggest the curated gene sequence referred to by the Examiner, for reasons already noted above and previously.

Regarding paragraph [0063], Applicant respectfully traverses the Examiner's interpretation that this represents curating comprising removal of commonly repeated subsequences. Masking can be incorporated into many different processes and is not to be equated with curating comprising removal of commonly repeated subsequences. For example, masking can be used to eliminate entire sequences from being selected for a process, and this would have nothing whatsoever to do with curating comprising removal of commonly repeated subsequences. It is respectfully submitted that paragraph [0063] of Zhou et al. mentions nothing of curating or of removing commonly repeated subsequences.

The Examiner further noted that Zhou et al. reports that the sequence is insufficiently complex with too many repeats to be uniquely and/or reliably represented by a probe set (paragraph 0126). However, this cannot be the case with the instant claims, as notification of at least one gene of interest is received from a customer, not merely a sequence, as in Zhou et al. Based on this, database searching is the performed to obtain sequence data for probe selection for the at least one gene of interest. The sequence data for use in probe selection obtained by the database searching is curated after the database searching. To clarify these distinctions, claims 1, 22 and 27 have been amended to recite these distinctions. Support for these amendments can be found, for example, at paragraph [0070] of the specification and throughout the specification.

The Examiner admitted that Zhou et al. (60/301,298) does not specifically state curating or curated sequence. The Examiner asserted that Markowitz et al. describe "manual data curation including detecting potential sequence data contamination (0043, 0046), and sequence searching for a user-provided nucleotide sequence against a database of GenBank sequences corresponding to Affymetrix (vendor) probe sets (0249)", which the Examiner interpreted to represent curating a

sequence and selecting at least one probe specific for a curated sequence. Applicant respectfully traverses. It is respectfully submitted that Markowitz et al. is directed to a system and method for providing a common interface for multiple databases, see Abstract, and has nothing to do with design or fabrication of arrays. The paragraphs [0043] and [0046] referred to by the Examiner describe methods for classifying gene fragments that may appear in a gene database, e.g., see paragraphs [0040]-[0041]. One method that may be employed in classifying gene fragments is manual curation, where gene fragments without a Unigene match are reviewed to detect potential sequence data contamination. Applicant does not claim to have invented the broad concept of curation. This manual curation described by Markowitz et al. has nothing to do with selection of probes or array design as claimed. Further, the present claims recite selecting at least one gene of interest, not a gene fragment. Nor does Zhou et al. appear to disclose notification of at least one gene of interest received from a customer.

It is respectfully submitted that the manual curation described by Markowitz et al. is carried out to classify certain gene fragments that have not been previously classified and is not carried out for probe selection, or for any use of the gene fragments other than classifying them, prior to any further use.

It is further respectfully submitted that Zhou et al. searches for previously existing probes already provided on arrays and/or is provided with sequence information from the client. In neither case would Zhou et al., whether or not modified by Markowitz et al., receive a selected gene of interest, perform database searching for sequence data for probe selection for the at least one gene of interest, and curate the sequence data for use in probe selection obtained by the database searching after the database searching.

With regard to claims 1, 3, 22, 27, 32 and 45, the Examiner asserted that the user modification of the design represents completion of the array design by the customer. Applicant respectfully traverses. Applicant finds no mention of these features in claims 10 and 11 of Zhou et al., contrary to the Examiner's assertions. Also, it appears that if the user rejects or modifies a proposed custom design, the system then goes back and generates another custom design and presents it to the user to repeat the approval process, e.g., see the Abstract.

The Examiner asserted that Cracauer et al. disclose a high-throughput oligonucleotide production system, designing and producing detection arrays for target sequences (paragraph [0434]), and receiving orders from a customer who enters a target sequence into a web interface ([0435, 0539]). It is respectfully submitted that paragraph [0435] is directed to mass producing designed assays based upon a customer's input of a target sequence. Paragraph [0539] describes an INVADERCREATOR module

that may be customized for a particular assay. In this instance, however, the user again must input a target sequence or code or number that causes retrieval of a sequence from a database, see paragraph [0540].

The Examiner asserted that Cracauer et al. described a curated sequence at paragraph [0484]. Applicant respectfully submits that paragraph [0484] describes Locus Link, which provides a single query interface to curated sequence and descriptive information about genetic loci, as is well-known in the art. Again, Applicant emphasizes here that Applicant is not claiming to have invented curating in general, but rather curating sequence data for probe selection, after obtaining such sequence data by database searching. Paragraph [0484] has nothing to do with this, since Locus Link searches a database of data that has already been previously curated.

The remaining paragraphs referred to by the Examiner pertain to in-silico analysis methods to analyze a candidate target sequence and sequence and sequence-related information databases, see paragraph [0444]. Accordingly, a candidate sequence is first input to the system, see paragraph [0445], and the candidate sequence is screened for repeat sequences, research artifact sequences, etc. Thus, these are all preliminary screening techniques for identifying a candidate sequence to be input to the system. Cracauer et al. does not teach, disclose or suggest inputting at least user selected gene to its system, database searching to obtain sequence data, and curating the obtained sequence data for probe selection, as is presently claimed in the instant independent claims. Accordingly, even if it were proper to combine Cracauer et al. with Zhou et al. and Markowitz et al. in the manner as suggested by the Examiner, which Applicant does not agree that such a combination would be proper, the resulting combination would still not meet the limitations of the independent claims.

Accordingly, in view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1-11, 22, 27-28, 31-37, 41-44 and 47-49 (claim 46 having been canceled) under 35 U.S.C. Section 103(a) as being unpatentable over Zhou et al., USPAP 2003/0120432 A1 in view of Markowitz et al., USPAP 2003/0100999 and Cracauer et al., USPAP 2007/0178474, as being inappropriate.

Conclusion

Applicants submit that all of the claims are in condition for allowance, which action is requested. If the Examiner finds that a telephone conference would expedite the prosecution of this application, please telephone the undersigned at 408-736-3554.

The Commissioner is hereby authorized to charge any underpayment of fees associated with this communication, including any necessary fees for extensions of time, or credit any overpayment to Deposit Account No. 50-1078, order number 10011076-1.

Respectfully submitted,

Date: 1/16/08

By: _____
Alan W. Cannon
Registration No. 34,977

Agilent Technologies, Inc.
Legal Department, DL429
Intellectual Property Administration
P.O. Box 7599
Loveland, CO 80537-0599